

1064-92-97

David Gurarie* (dxg5@case.edu), Math. dep., CWRU, Cleveland, OH 44106. *Stochastic within-host models of malaria infection: calibration and Agent-Based Communities.*

Agent-based modeling of malaria infection offers an attractive alternative to the conventional population-based methodology. It allows to accommodate heterogeneous 'host-vector-parasite' populations and realistic transmission environment. To build such community model one need a suitable within-host model (agent) that accounts for host immunity and parasite regulation. Immune response involves a complex array of multiple cell-types, signaling/effector proteins and cascading processes. Other complexities arise from immune-evasion strategies by many parasites, like malaria P-falciparum. Stochastic processes are useful for representing such complex dynamics. We outline several within models ranging from a simple 3-state system, to more detailed versions. All of them can be efficiently manipulated (mathematically and computationally) to allow numeric experiments with large host ensembles' and communities'. Some of these models were calibrated using malaria-therapy data. We explain the details of calibration. The resulting choices of within-host' parameters provide us the basic building blocks for Agent-based Communities (ABC). We demonstrate a few examples of such ABC, and look in particular at the effect of transmission intensity on the resulting patterns of parasitemia. (Received August 31, 2010)